

Fig. 1

FASTA "BEB02660"

ICTB : 1 ATGACTGCTGCGCAACTCTGACTTTTGCCCATTACCACCCCAACAGTGGGGCCACAGC 60 (SEQ ID NO:2)
 || || ||||| | | |||| | |||| | |||| | |||| | |||| | ||
 SLR : 13 ATCTCTATCTGGCGATCGCTGATGTTTGGCGGTTTTCCTCCCCCAGGAATGGGGCCGGGGC 72 (SEQ ID NO:4)

 ICTB : 61 AGTTTCTTGCCATCGGCTGTTTGGCAGCCTGC-GAGCTTGGCGGGCCTCCAGCCAGCTGTT 119
 ||| | | ||||| || | |||| | | |||| | |||| | |||| | |||| |
 SLR : 73 AGTGTGCTCCATCGTTTGGTGGGCTGGGACAGAG-TTGGATACAGGCTAGTGTGCTCTG 131

 ICTB : 120 GGTTTGGTCTGAGGCACCTGGGT--GGCTTCTTGCTTGCTGTCGTCTACGGTTCGGGCTCCG 177
 | | ||||| ||||| |||| | |||| | |||| | |||| | |||| | |||| |
 SLR : 132 GCCCCACTTCGAGGCCATTGGGTACGGCT-CTAG-TGGCAATAATTTTATTGCGGCTCCC 189

 ICTB : 178 TTTGTGCCCCAGTTCCGCCCTAGGCTTGGGCTAGCCCGCATCGCG-GCCTATTGGGGCCCT 236
 || | |||| | || | |||| | |||| | |||| | |||| | |||| | ||
 SLR : 190 TTCACCTCCACACCACATGTTGGCCATTTTAT-GCTGCTCTGTGGAGCCCTTTTGGGCTCT 248

 ICTB : 237 GCTCTCGCTGACAGATATCGATCTCGGGCAAGCA--ACCCCATTCACCTGGTGGTGT 293
 ||| | | | |||| | || | |||| | |||| | |||| | |||| | |||| |
 SLR : 249 GCTGACCTTTGCTGAT--CAACCAG-GGAAGGTTTGACTCCCATCCATGTTTGTAGTTT 305

 ICTB : 294 GCTCTACTGGGGCGTCGATGCCCTAGCAACGGGACTCTCACCCGTACCGCTGCAGCTTT 353
 ||||||| || | || | |||| | |||| | |||| | |||| | |||| | |||| |
 SLR : 306 TGCCTACTGGTGCAATTCGGCGGATCGCCGTGGGATTTTCTCCGGTAAATAATGGCGCGGC 365

 ICTB : 354 AGTTGGGCTAGCCAAACTGAC-GCTC-TACCTGTGTGTTTTCCTGCTGCTGCTGCTGCTGCT 411
 ||| |||| | || | |||| | |||| | |||| | |||| | |||| | |||| |
 SLR : 366 GTCGGGTTAGCGAAATTAACAGCTAATTTATGCTGTTTCTAC--TGGCGCGCGAGGTTA 423

 ICTB : 412 CTCCGCAATCCCCGCTGTC-GATCGCTGCTGTTCTCGGTCGTCGTGATCACATCGCTTTT 470
 | | || | | |||| | || | |||| | |||| | |||| | |||| | |||| |
 SLR : 424 TTGCAAAACAAACAATGGTTGAAC-CGGTTAGTAACCGTTGTTTACTGGTAGGGCTATT 482

Fig. 2

ICTB : 471	TGTCAGTGTCTACGGCCTCAACCAATGGATCTACGGCGTTGAAGAGCTGGCGACTTGGGT	530
SLR : 483	GGTGGGAGTTACGGTCTGCGACAACAGGTGGACGGGTAGAACAGTTAGCCACTTGGAA	542
ICTB : 531	GGATCGCAACTCGGTTGCCGACTTCACCTCACGGGTTTACAGCTATCTGGCAACCCCAA	590
SLR : 543	TGACCCCACTCTACCTTGCCCCAGGCCACTAGGGTATATAGCTTTTTAGGTAATCCCAA	602
ICTB : 591	CCTGCTGGCTGCTTATCTGGTGCCGACGACTGCCCTTT-CTGCAGCAGCGATCGGGTGT	649
SLR : 603	TCTCTTGGCGGCTTACCTGGTGCCCATGACGGGTTTGAGCTTGAGT-GCCCTGGTGGTAT	661
ICTB : 650	GGCGGGCTGGCTCCCCAAGCTGCTGGCGATCG-CTGCGACAGGTGCGAGCAGCTTATGT	708
SLR : 662	GGCGACGGTGGTGCCCCAAACTGCTGG-GAGCAACCATGGTGATGTTAACTACTCTGT	720
ICTB : 709	CTGATCCTCACCTACAGTCGCCGGTGGCTGGCTGGGTTTGTGCCCATGATTTTGTCTGG	768
SLR : 721	CTCTTTTACCAGAGCGCGGGCGGTGGCTAGCAGTGCTGGCCCTGGGAGCTACCTTC	780
ICTB : 769	GCGTTATTAGGGCTCTACTGGTTTCAACCCCGTCTACCCGACCCCTGGCGACGCTGGCTA	828
SLR : 781	CTGGCCCTTGTACTTCTGGTGGTTACCCCAATTACCCAAATTTGGCAACGGTGGTCT	840
ICTB : 829	TTCCCAGTCGATTTGGGTGGACTAGTCGCGGTGCTCTT-GGTGCGGTGCTTGGACT---	884
SLR : 841	TTGCCCCCTGGC----GATCGCC--GTGGCGGTATATTAGGTGGGGGAGCGTTGATTGCG	894
ICTB : 885	-TG-AGCCGTTGCGCGTGGCGGTGTGAGCATCTTTGTGGGGCGTGAAGACAGCAGCAAC	942
SLR : 895	GTGGAACCGATTCCGACTCAGGGCCATGAGCATTTTGTCTGGCGGGAAGACAGCAGTAAT	954

Fig. 2

[illegible]

Fig. 2

+++W++L F + PQ+WG S IHR L G ++W +S L EALG L+A+++ +APF
 SLR : 5 ISIWRSLMFGGFSQPQEWGRGSLHRLVGVWGQSWIQASVLNPHFEALGTALVAIIFIAAPF 64

ICTB : 61 VESSALGLGLAAIAYWALLSLTDIDLRQATPIHNLVLLYWGVDALATGLSPVRAAALVG 120
 ++ LG+ + A+WALL+ D + TPIH LV YW + A+A G SPV+ AA G
 SLR : 65 TSTTMLGIFMLLCCGAFWALLTFADQPGKGLTPIHVLVFAYNCISAIAVGFSFVKMAAASG 124

ICTB : 121 LAKLTLYLLVFALAAARVLRNPRLSLLFSVVVITSLFVSVYGLNQWYGVVEELATWVDNRN 180
 LAKLT L +F LAAR+L+N + + L +VV++ L V YGL Q + GVE+LATW D
 SLR : 125 LAKLTANLCLFLLAARLLQNKQWLNRVLTVLLYGLLVGSYGLRQQQVDGVEQLATWNDPT 184

ICTB : 181 SVADFTSRVSYLGNPNLLAAYLVPTTAFSAAAIGVMRGWLPKLLAIAATGASSLCLILT 240
 S +RVYS+LGNPNLLAAYLVP T S +A+ VWR W PKLL + LCL T
 SLR : 185 STLAQATRVSSELGNPNLLAAYLVPMTGLSLSALVVWRRWPKLLGATMVIVNLLCLFFT 244

ICTB : 241 YSRGGWLGFWAMIFVWALLGLYWFQPRLPAPWRRNLFPVVLGGLVAVLLVAVLGLEPLRV 300
 SRGGWL +A+ + L +W+ P+LP W+RW P+ + V + A++ +EP+R+
 SLR : 245 QSRGGWLAVALGATFLALCYFWWLPLQPKFWQWNSLPLAIAVAVILGGGALIAVEPIRL 304

ICTB : 301 RVLSIFVGREDSSNNFRINWNLAVLQMIQDRFWLIGPGNTAFNLVPLYQQARFTALSA 360
 R +SIF GREDESSNNFRINWV V MI+ RP +GIGPGN AFN +YP Y + RFTALSA
 SLR : 305 RAMSIFAGREDSSNNFRINWVEGVKAMIRARPIIGIGPGNEAFNQIYPYMYMRPRFTALSA 364

ICTB : 361 YSVPLEVAVEGGLGLTAFAWLLLVTAVTAVRQVSRRLRRDRNPQAFWLMASLAGLAMLG 420
 YS+ LE+ VE G++G T WLL VT V V R R+ P+ W+M +LA + G+L
 SLR : 365 YSIYLEILDVETGVVGFTCMLNLLAVTLGKGVELVKRCRQTLAPEGIWMGALAAIIGLLV 424

ICTB : 421 HGLFDTVLYRPEASTLWNLICIGAIASFQOPQPSKQLPPEAEHSDEKM 467
 HG+ DTV YRP STLWNL + +AS W ++ + E+ D+ +
 SLR : 425 HGMVDTVWYRPPVSTLWNLVVAIVASQWASQAARLEASKEENEDKPL 471

Fig. 3

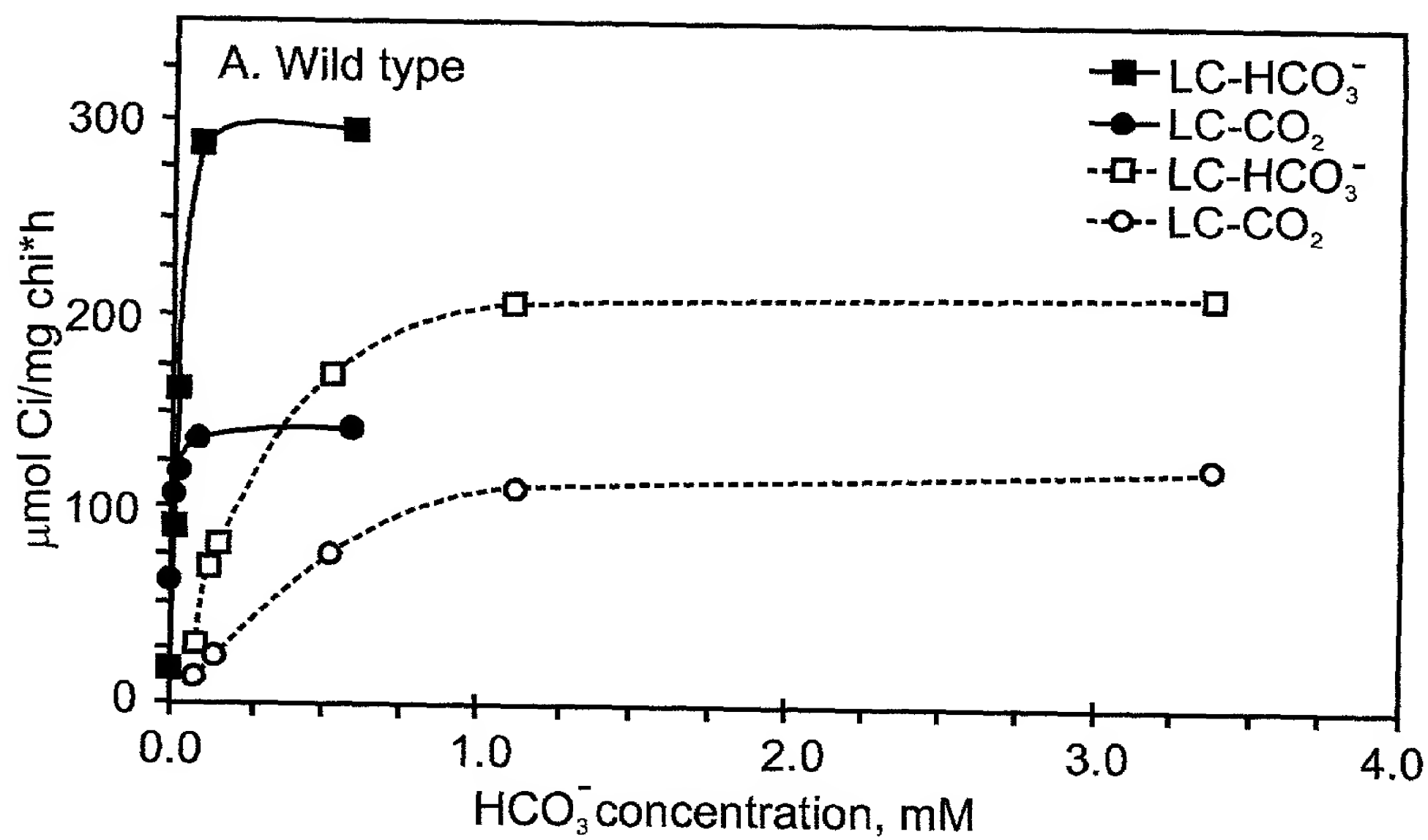


Fig. 4a

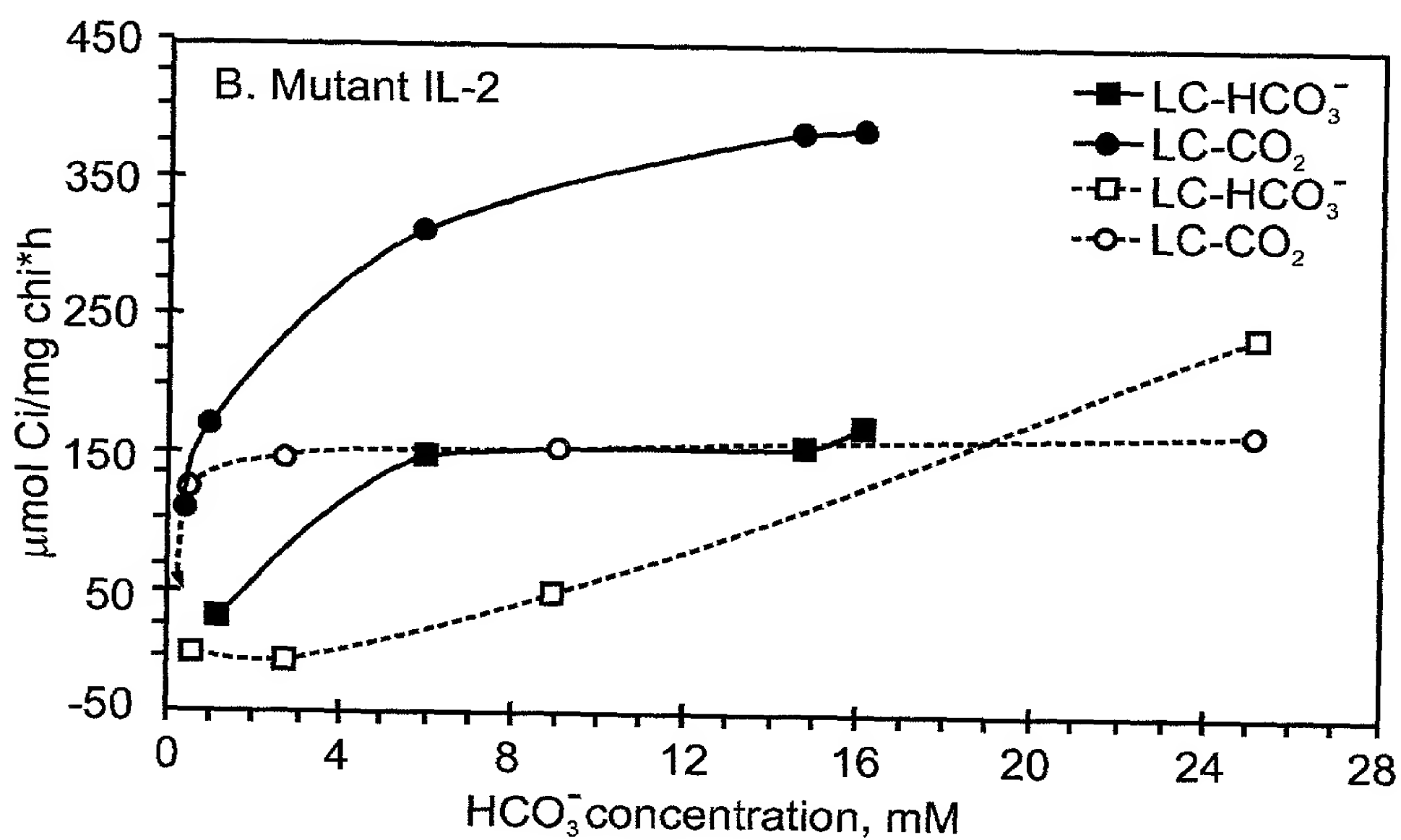


Fig. 4b

Wild type	GGGCT-AGCCGGGATCGCGGCTATTGGGCCC	(SEQ ID NO: 6)
IL-2 ApaI side	GGGCT-AG--G-GATCGC-GCCTATTGGGCCC	(SEQ ID NO: 7)
IL-2 BamHI side	GGGCTCA-----GATCGC-GCCTATTGGGCCC	(SEQ ID NO: 8)
IctB	G L A A I A A Y W A L	(SEQ ID NO: 9)

Fig. 5

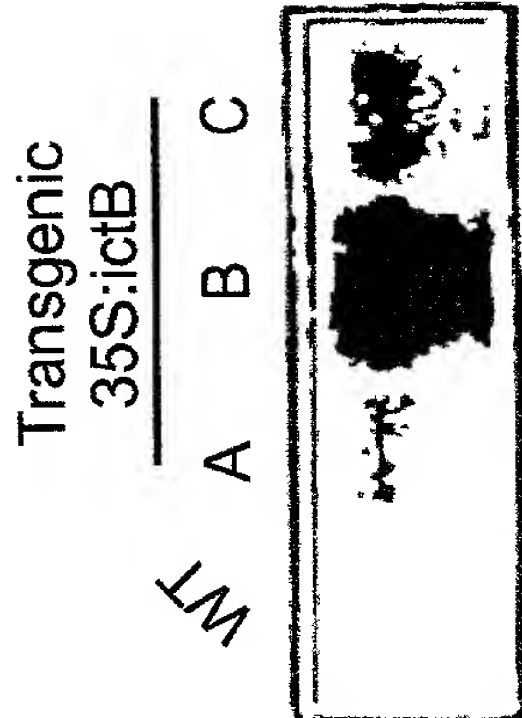


Fig. 6